

STIC Database Tracking Number: 240590

To: BAO LI
Location: REM-3D24 / Mailbox 3C18
Art Unit: 1648
Thursday, October 18, 2007

Case Serial Number: 10/789355

From: TOBY PORT
Location: EIC 1600
REM-1D58 / REM-1A59
Phone: (571)272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner LI:

Enclosed are the results for the alignment portion of your sequence search. The results for Seq ID 30 translated and edited should be in SCORE on Monday. If you have any questions, please don't hesitate to call me.

Thank you for using STIC search services.

Toby Port
x22523

GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: October 18, 2007, 17:20:08 ; Search time 5 Seconds
(without alignments)
36.902 Million cell updates/sec

Title: US-10-789-355A-30
Perfect score: 9605
Sequence: 1 gccagcccccagattgggggc.....ggcctctctgagatcaagt 9605

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 9605 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : aj238799.gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9605	100.0	9605	1	HCJ238799
2	33.4	0.3	9605	1	HCJ238799

ALIGNMENTS

RESULT 1
HCJ238799
LOCUS Hepatitis C virus type 1b complete genome, isolate Conl.
ACCESSION AJ238799
VERSION AJ238799.1 GI:5420376
KEYWORDS complete genome; core protein; glycoprotein E1; glycoprotein E2; NS2 proteinase; NS3 proteinase/helicase; NS3/4A proteinase cofactor; NS4b protein; NS5A phosphoprotein; NS5B RNA dependent RNA polymerase; p7 peptide; polyprotein.
SOURCE Hepatitis C virus subtype 1b
ORGANISM Hepatitis C virus subtype 1b
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
REFERENCE 1
AUTHORS Lohmann, V., Korner, F., Koch, J., Herian, U., Theilmann, L. and Bartenschlager, R.
TITLE Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line
JOURNAL Science 285 (5424), 110-113 (1999)
PUBMED 10390360
REFERENCE 2 (bases 1 to 9605)
AUTHORS Bartenschlager, R.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-1999) Bartenschlager R., Institute for Virology, Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67,

FEATURES
source

55131 Mainz, GERMANY
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RESULT 2

RESULT 2
HCJ238799/c

HCJ238/99/C
LOCUS

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DEFINITION
ACCESSION

ACCESSION
VERSION

KEYWORDS

KEYWORDS

COPYRIGHT

SOURCE
ORPCANTCM

ORGANISM

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1
AUTHORS
Lohmann,V., Korney,F., Koch,J., Herian,U., Theilmann,L. and Bartschlagler,R.
TITLE
Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line
JOURNAL
Science 285 (5424), 110-113 (1999)
PUBMED
10390360
REFERENCE 2 (bases 1 to 9605)
AUTHORS
Bartschlagler,R.
TITLE
Direct Submission
Submitted (10-MAY-1999) Bartschlagler R., Institute for Virology, Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67, 55131 Mainz, GERMANY

FEATURES
source

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GenCore version 6.2.1
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 18, 2007, 17:16:54 ; Search time 9 Seconds
(without alignments)
4.698 Million cell updates/sec

Title: US-10-789-355A-30
Perfect score: 17788
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1 seqs, 2201 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-OUT=seq30-seq4.res -SIMRANGE=0.0005 -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1 -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZ=0 -MINLEN=0 -MAXLEN=200000000 -NCPU=6
-NO XLPXY -NEG SCORES=0 -LONGLOG -MINDIST=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database : seq4.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	131.5	0.7	2201	1	US-10-789-355A-4

ALIGNMENTS

RESULT 1
US-10-789-355A-4
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; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083-3-D2
; CURRENT APPLICATION NUMBER: US/10789,355A
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 10/029,907
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 30

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Db 1121 SerProThrHisTyrValProGluSerAspAlaAlaAlaArgValThrGlnIleLeuSer 1140
QY 6189 AGCTTTACCATCACTCAGCTCTGAGAGGCTTACAGCTGATGATCAACGAGGACGCTCC 6248
Db 1141 SerLeuThrIleThrGlnLeuLeuIysArgLeuHisGlnTrpIleAsnGluAspCysSer 1160
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QY 6309 GATTTCAGACCTGGCTCAGTCCAGCTCTCGCGGATTCGCGGAGTCCCTCTCTTC 6368
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 Db 285 LysGlyProIleThrGlnMetTyrThrAsnValAspGlnAspLeuValGlyTrpGlnAla 304
 Qy 8737 -----CTTTGGCAGATGATCGTGGCGACCTGACACATG----- 8702
 Db 305 ProProGlyAlaArgSerLeuThrProCysThrCysGlySerSerAspLeuTyrLeuVal 324
 Qy 8701 --GAGGAGCATGATGTTATC----- 8684
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 Db 405 SerSerProProAlaValProGlnThrPheGlnValAlaHisLeuHisAlaProThrGly 424
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 Db 425 --SerGlyLysSerThrLysValProAlaAlaTyrAlaAlaGlnGlyTyrLysValLeu 443
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 Db 500 AlaTyrAspIleIleIleCysAspGluCysHisSer----- 511
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 Db 512 -----ThrAspSerThrThrIleLeuGlyIleGlyThr 522
 Qy 8202 CGACCCGCTGTCCAGGAGATTTGGAATCCGTATG-----AAGAGCCCATCAGCGCT 8149
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 Qy 7428 CGCTGT----- 7423
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 Db 750 GluSer-----ValPheThrGlyLeuThrHisIleAspAla 761
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 Db 814 -----ProLeu-----LeuTyrArgLeuGlyAlaVa 822
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Db	875	-----GlyArgIleLeuSerGly***ProAlaIleIleProAspArgI	890
Qy	6897	CCGTCTCCCGCTAATGTGGAGGGGTGGGATCGAATGGAATGAGCAGCTCTACGCTCG	6838
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Db	1107	-----	1107
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Db	1108	-----AsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrV	1126
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Db 1468 -----ArgSerArgLysPheProArgAlaMetProIleTyr 1479
Qy 4848 TCA-----CAAACCTGTAATGCCCA----- 4828
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Qy 4667 ----- 4667
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Db 1600 SerGluGluAlaSerGluAspValValCysCysSerMetSerTyrThrTrpThrGlyAla 1619
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Qy 4592 -----ATATGCTACAGCATTTGAGTCCGAGCGCGGACAGCTTCGCGGC 4551
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Qy 4550 GAGCTCATCACAATTT----- 4536
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Qy 4535 -----CTTCTTGGAAATGGCAGAAAT----- 4515
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Db 1955 -----ArgTyrSerAlaProProGlyAspProProLysProGluTyrAspLe 1970
Qy 3806 GGGGAGAGTAGGCTCCCTGCTGCTGCCCGCGCGCGCAGCGGAATGATCGCATG 3747
Db 1970 uGlu----- 1971
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Db 1972 -LeuIleThrSerCysSerSerAsnValSerValAlaHisAspAlaSerGlyLysArg-- 1990
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Db 1991 -----ValTyrLeuThrArgAs 1997
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Db 1997 pProThrThrProLeuAlaArg-----AlaAlaTrpGluThrAlaArgHisTh 2013
Qy 3569 GCCATTGACGCGAGTCCGCCAGGAAGATTGTGTGCGGTGGAGACCACTTTGACC----- 3515
Db 2013 rProVal-----AsnSerTrpLeuGlyAs 2021
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Db 2021 nIleIleMetTyrAlaProThrLeuTrp-----AlaArgMetIleLeuMe 2036

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Db 2036 t 2036

Search completed: October 18, 2007, 17:17:24
Job time : 24.5 secs

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 640 650 660 670 680 690 700
 1640 1650 1660 1670 1680 1690 1700
 TCNACTGCTTCTTCTGCTGCTTCTAGCTGCACAAAGTTCAACT-CATCTGGATGCCAGAGCGCATG
 |||||
 TGCTCTGCGGAGAAATGATCATCATGCTGATGCTGATGCGGGCTGATACGGTTGATCCGGCTACTG
 710 720 730 740 750 760 770
 1710 1720 1730 1740 1750 1760 1770 1780
 GCGAGTGCAGCCCATCGAGCTGCTGCTGAGGGTGGGGGCCCATCACTACATAGTACACAGCTCG
 |||||
 CCATTCGACCAACGAGCAACATCGATC-----GAGCGAGCAGCTACTCGATGGAGGCGGTCT
 780 790 800 810 820 830 840
 1790 1800 1810 1820 1830 1840 1850
 GACGAGGCTTATTTGTTGGCACTACGACCCCGCTGCGGTATCGTACCGCGGCGAGTGTGTGT
 |||||
 TGTGATCAGGATGATCTGGAGAGAGCATAGGGGCTCGCCCGAGCCGAACTGTTCCGACGCTCAAGGC
 850 860 870 880 890 900 910
 1860 1870 1880 1890 1900 1910 1920
 CCACTGCTGCTTCAACCCAGCCCTGCTGCTGGGACGACCCGCTTCCGCTCCCTACCTACAGT
 |||||
 GC-----GCATGCCGACGCGAGGATCTGCTGATGACCACTGCGGATGCTCTTCCCGAATATC
 920 930 940 950 960 970
 1930 1940 1950 1960 1970 1980 1990
 TGGGGGAGATGAGAGGAGCTGCTTCTTAAACACGCGGCGCGGCAAGCAACTGCTTTGGCTGT
 |||||
 ATGTTGGAATATGCGGCTTTCTGGAATTCATCGACTGTGGCGGCTGGGTGGCGGACCGCTATCAGGAC
 980 990 1000 1010 1020 1030 1040
 2000 2010 2020 2030 2040 2050 2060
 ACATGATGATGAGTGGTTTCAACAGACGCTGGGGGCCCCCGGTATACATGGGGGATCGGCAAT
 |||||
 ATAGCGTGGCTACCGCTGATATGCTGAAGACTTGGCGGCGAATGGGCTGACCCGCTTCTCGTGTCTTAC
 1050 1060 1070 1080 1090 1100 1110
 2070 2080 2090 2100 2110 2120 2130 2140

3. US-10-789-355A-30 (1-9605)
 US-10-789-355A-1 Sequence 1, Application US/10789355A

Initial Score = 6838 Optimized Score = 7416 Significance = 1.37
 Residue Identity = 86% Matches = 7525 Mismatches = 1098
 Gaps = 98 Conservative Substitutions = 0

AAACCTTGACCTGCGCCCAACGAGCTGCTCCGGAAGACCCCGAGGCGCACTTACACCAAGTGTGGTTCGGGG
1120 1130 1140 1150 1160 1170 1180 1190
GGTATCGCGCTCCCGAATTCGAGGCGATCGCTTCTATCGCCTTCTTGACGAGTCTTCTTGAGTTCGCGCC
2150 2160 2170 2180 2190 2200 2210
CCTTGGTGTGACA-CCAGATGCTTGGTTCACCTACCCATACAGGCTTGGCACTACCCCTGCATGTCAACTT
2220 2230 2240 2250 2260 2270 2280
TACCATCTTCAAGTTAGATGATAGCTGGGGGAGTGGAGCAGAGCTCGA--AGCGCATGCAATTGAGACT
GAAGCGCTTGGAAATAAGGCGGCTGTGCTGTATATGTTATTTTCCACCATATGCGCTCTTTTGGCA
1270 1280 1290 1300 1310 1320 1330
2290 2300 2310 2320 2330 2340 2350
CGAGAGAGCGTTGTAACTTGG---AGGACAGGACAGATCAGAGCTTAGCCGCTGTCTCTGTCTATCAACG
ATGTGAGGCGCCGGAAACCTGCGCTGTCTTGTACGAGCAATTCCTAGGGGTCTTTCCCTCTCGCCAAAG
1340 1350 1360 1370 1380 1390 1400
2360 2370 2380 2390 2400 2410 2420
GAGTGGCAGGATTCGCCCTTTCCTTACCACCTACCGCTCTGTCCACTGTGTTGATCCATCTCCATCAG
GAAATGCAAGGTCTGTTGAATGTCGTGAAGAGC-----AGTTCTCTGAAGCTTCTTGAAGACAAAC
1410 1420 1430 1440 1450 1460 1470
2430 2440 2450 2460 2470 2480 2490
AACGTGCGGACGTACAACTGTAAGGTATAGGTC-----GGCGTGTCTCTTTCGAATCAAATGAGG
AACGTGCTGTAGGACCTTTGACGAGCGGAAACCCCACTGCGGACAGAGTGTCTCTCGCGCCAAAGCC
1480 1490 1500 1510 1520 1530 1540
2500 2510 2520 2530 2540 2550 2560
AGTATGCTGCTGTCTTCTTCTTCTGCGGACGCGCGCTGTGCTGTGTGGATGATGCTGTGA
ACGTGTATAAGATACACTGCAAGGCGGCAACCCAGTGCACCTGTGAGT-TGGATAGTTGTGGAA
1550 1560 1570 1580 1590 1600 1610
2570 2580 2590 2600 2610 2620 2630
TAGCTCAAGCTGAGCGCGCTTAGAAGAACCTGTGTCTCAACGCGGCATCGTGC CGGGCGCATGCA
GAGTCAAAATGGCTCTCCTCAAGCGTATTCAACAAAGGCGCTGAAGGATGC-----CCAGAG
1620 1630 1640 1650 1660 1670
2640 2650 2660 2670 2680 2690 2700
TTCTCTCCTTCTCGTGTCTTCTGTGTGCTGCTGTATCAATCAAGGCGAGGCTGTCTCTCGGGCGCATATG
GTACCCCATGTATGGATCTGATCTGCGGCGCTCGGTGACATGCTTTACATGTGTTTGTAGTCGAGGTTAAA
1680 1690 1700 1710 1720 1730 1740
2710 2720 2730 2740 2750 2760 2770
CCCTTAGCGGTATGGCGCTACTCCTGCTCTGCTGCGGTACCAACAGGCGATACCCATGAGACGGG
AACGTCTAGGCCCCCGAACACGAGGCGTGGTTTCTTTGAAAACAGATATA--CCATGAGACGGG
1750 1760 1770 1780 1790 1800 1810
2780 2790 2800 2810 2820 2830 2840 2850
AGATGGCAGCATCGTGGAGGCGCGGTTTTCGTAGGTCTGATCTGTGACCTTGTACCGCATATAGC
AGATGGCAGCATCGTGGAGGCGCGGTTTTCGTAGGTCTGATCTGTGACCTTGTGACCGCATATAGC
1820 1830 1840 1850 1860 1870 1880
2860 2870 2880 2890 2900 2910 2920
TGTTCTCGCTAGGCTCATATGTTGTTTACAAATATTTTATCACAGGCGGAGCAGCATTTGCAAGTGTGA
TGTTCTCGCTAGGCTCATATGTTGTTTACAAATATTTTATCACAGGCGGAGCAGCATTTGCAAGTGTGA
1890 1900 1910 1920 1930 1940 1950
2930 2940 2950 2960 2970 2980 2990
TCCCCCCTCAACGTTCGGGGGGCGGATGTCCTCTCTCAGTGCAGATCCACCCAGAGCTAA

TCCTCCCTCAACAGTTCGGGGCGCGATGCCGTATCCTCTCAGTGCAGATCCACCCAGAGCTAA
1960 1970 1980 1990 2000 2010 2020
3000 3010 3020 3030 3040 3050 3060
TCCTTACCATCACCAAAATCTTGTCTCCCATACTCGTCCCACTCATCTGTCAGGCTGTATACCAAG
TCCTTACCATCACCAAAATCTTGTCTCCCATACTCGTCCCACTCATCTGTCAGGCTGTATACCAAG
2030 2040 2050 2060 2070 2080 2090 2100
3070 3080 3090 3100 3110 3120 3130
TGCGTACTTCTGTCGCGCACAGGCTCATCTGTCATGTCATCTGTCGGAAGTTCGTGGGTCAAT
TGCGTACTTCTGTCGCGCACAGGCTCATCTGTCATGTCATCTGTCGGAAGTTCGTGGGTCAAT
2110 2120 2130 2140 2150 2160 2170
3140 3150 3160 3170 3180 3190 3200 3210
ATGTCCAAATGGCTCTCATGAGTTGGCGCATGACAGGTACGTATGATGACCATCTCAACCCACTGC
ATGTCCAAATGGCTCTCATGAGTTGGCGCATGACAGGTACGTATGATGACCATCTCAACCCACTGC
2180 2190 2200 2210 2220 2230 2240
ATGTCCAAATGGCTCTCATGAGTTGGCGCATGACAGGTACGTATGATGACCATCTCAACCCACTGC
3220 3230 3240 3250 3260 3270 3280
GGACTGGTCCACCGCGCTTACGAGACTTGGGTGGCAGTTGAGCCGTGCTCTCTGATATGAGA
GGACTGGTCCACCGCGCTTACGAGACTTGGGTGGCAGTTGAGCCGTGCTCTCTGATATGAGA
2250 2260 2270 2280 2290 2300 2310
3290 3300 3310 3320 3330 3340 3350
CCAAAGTTATCCTGCGGGGCGAGACACCGCGGTGTGGGACATCATCTTGGGCTCGCCCTCGCGCC
CCAAAGTTATCCTGCGGGGCGAGACACCGCGGTGTGGGACATCATCTTGGGCTCGCCCTCGCGCC
2320 2330 2340 2350 2360 2370 2380
3360 3370 3380 3390 3400 3410 3420
GCAGGGGAGGAGATACATCTGGGACCGGAGACAGCTTGAAGGCGAGGTTGGGACATCTCTCGGCTA
GCAGGGGAGGAGATACATCTGGGACCGGAGACAGCTTGAAGGCGAGGTTGGGACATCTCTCGGCTA
2390 2400 2410 2420 2430 2440 2450 2460
3430 3440 3450 3460 3470 3480 3490
TTACGGCTTACTTCCCAACAGACGCGAGGCTTACTTGGCTGATCATCATCTGCTCAGCGCGGACAGA
TTACGGCTTACTTCCCAACAGACGCGAGGCTTACTTGGCTGATCATCATCTGCTCAGCGCGGACAGA
2470 2480 2490 2500 2510 2520 2530
3500 3510 3520 3530 3540 3550 3560 3570
ACCAAGTCCGAGGGGAGTCCAGTGTCTCCACCGCAACAAATCTTCTTGGGACCTTGGTCAATGGCG
ACCAAGTCCGAGGGGAGTCCAGTGTCTCCACCGCAACAAATCTTCTTGGGACCTTGGTCAATGGCG
2540 2550 2560 2570 2580 2590 2600
3580 3590 3600 3610 3620 3630 3640
TGTTTGGACTGTCTATCATGTGTCGCGCTCAAGACCTTCCGCGCCCAAGGCGCAATCAACCAATGT
TGTTTGGACTGTCTATCATGTGTCGCGCTCAAGACCTTCCGCGCCCAAGGCGCAATCAACCAATGT
2610 2620 2630 2640 2650 2660 2670
3650 3660 3670 3680 3690 3700 3710
ACACCAATGTGGACAGGACTCGTGGCTGGCAAGCGCCCGGGCGGCTTCTTGTGACCATGACCT
ACACCAATGTGGACAGGACTCGTGGCTGGCAAGCGCCCGGGCGGCTTCTTGTGACCATGACCT
2680 2690 2700 2710 2720 2730 2740
3720 3730 3740 3750 3760 3770 3780
GCGCAGCTCGGACTTACTTACTTGTGTCAGGAGCATGCGATGTCAATCGGTGCGCGGGCGGACAGCA
GCGCAGCTCGGACTTACTTACTTGTGTCAGGAGCATGCGATGTCAATCGGTGCGCGGGCGGACAGCA
2750 2760 2770 2780 2790 2800 2810 2820
3790 3800 3810 3820 3830 3840 3850
GGGGAGCTTACTTCTCCCGAGGCGGCTCTCTACTTGAAGGGCTTTCGGGGCGGCTCCATGCTTGGCCCT

3720 3730 3740 3750 3760 3770 3780
CGGAGCTCGACCTTTACTTGGTCAAGGAGATCGATGATTCCTCGGTGCGCGGGGCGACAGCAG
CGGAGCTCGACCTTTACTTGGTCAAGGAGATCGATGATTCCTCGGTGCGCGGGGCGACAGCAG
2750 2760 2770 2780 2790 2800 2810 2820
3790 3800 3810 3820 3830 3840 3850
GGGAGCCTACTCTCCCGACCGCTCTCTCTTAATTGAAGGGCTCTTCGGGGGTCCACTGCTCTGCCCTC
GGGAGCCTACTCTCTCCCGACCGCTCTCTCTTAATTGAAGGGCTCTTCGGGGGTCCACTGCTCTGCCCTC
2830 2840 2850 2860 2870 2880 2890
3860 3870 3880 3890 3900 3910 3920 3930
GGGAGCCTACTCTCTCCCGACCGCTCTCTCTTAATTGAAGGGCTCTTCGGGGGTCCACTGCTCTGCCCTC
GGGAGCCTACTCTCTCTCCCGACCGCTCTCTCTTAATTGAAGGGCTCTTCGGGGGTCCACTGCTCTGCCCTC
2900 2910 2920 2930 2940 2950 2960
3940 3950 3960 3970 3980 3990 4000
CGTGGAGTCTATGGAACCACTATGCGGTCCCGGTCTTCACGGCAACTCGTCCCTCGGGCCGTACCGCA
CGTGGAGTCTATGGAACCACTATGCGGTCCCGGTCTTCACGGCAACTCGTCCCTCGGGCCGTACCGCA
2970 2980 2990 3000 3010 3020 3030
4010 4020 4030 4040 4050 4060 4070
GACATTCAGGTGCGCCATCTACACGCCCTACTGCTAGCGGCAAGCACTAAGGTGCGGGTATGTC
GACATTCAGGTGCGCCATCTACACGCCCTACTGCTAGCGGCAAGCACTAAGGTGCGGGTATGTC
3040 3050 3060 3070 3080 3090 3100
4080 4090 4100 4110 4120 4130 4140
AGCCCAAGGTATAGGTGCTTCTGAAACCGCTCGGTGCGCGCACCTAGGTTCGGGGGTATATGTC
AGCCCAAGGTATAGGTGCTTCTGAAACCGCTCGGTGCGCGCACCTAGGTTCGGGGGTATATGTC
3110 3120 3130 3140 3150 3160 3170 3180
4150 4160 4170 4180 4190 4200 4210
TAAGCAGATGATCGACCTTAACATCAGAACCGGGTAAGGACCATCAACCGGTGCGCCCATCAGTA
TAAGCAGATGATCGACCTTAACATCAGAACCGGGTAAGGACCATCAACCGGTGCGCCCATCAGTA
3190 3200 3210 3220 3230 3240 3250
4220 4230 4240 4250 4260 4270 4280 4290
CTCCACCTATGCGAAGTTCTTTCGCGAGCGGTGCTCTGCGGGCGCTTATGACATCAATATATGATGA
CTCCACCTATGCGAAGTTCTTTCGCGAGCGGTGCTCTGCGGGCGCTTATGACATCAATATATGATGA
3260 3270 3280 3290 3300 3310 3320
4300 4310 4320 4330 4340 4350 4360
GTGCCACTCAACTGACTCGACCACTATCTTGGGCATCGGCACATGCTCGAACCGGAGCGGTGGAGC
GTGCCACTCAACTGACTCGACCACTATCTTGGGCATCGGCACATGCTCGAACCGGAGCGGTGGAGC
3330 3340 3350 3360 3370 3380 3390
4370 4380 4390 4400 4410 4420 4430
GCGACTGCTGCTCGACCGCTAGCGCTCGGGATCGGTACCGTCCGATCCCAACATCGAGGAGGT
GCGACTGCTGCTCGACCGCTAGCGCTCGGGATCGGTACCGTCCGATCCCAACATCGAGGAGGT
3400 3410 3420 3430 3440 3450 3460
4440 4450 4460 4470 4480 4490 4500
GGCTCTGCGACGATCGAGAAATCCCTTTTATGCAAGCATCCCATCGAGACCATCGAGGGGGAG
GGCTCTGCGACGATCGAGAAATCCCTTTTATGCAAGCATCCCATCGAGACCATCGAGGGGGAG
3470 3480 3490 3500 3510 3520 3530 3540
4510 4520 4530 4540 4550 4560 4570
GCACCTATTTCTGCGATTCAGAGAAATGATGATGCTCGCGGAGGTGTCGGCTCGGATCTCA
GCACCTATTTCTGCGATTCAGAGAAATGATGATGCTCGCGGAGGTGTCGGCTCGGATCTCA
3550 3560 3570 3580 3590 3600 3610

4580 4590 4600 4610 4620 4630 4640 4650
TGCTGTAGCATATTAACCGGGCTTTATCGGTATCGGTATACCAATAGCGGAGCGTATGTCGTAGCAAC
TGCTGTAGCATATTAACCGGGCTTTATCGGTATCGGTATACCAATAGCGGAGCGTATGTCGTAGCAAC
3620 3630 3640 3650 3660 3670 3680
4660 4670 4680 4690 4700 4710 4720
GGAAGCTTAATAGCGGGCTTTACCGGCGATTCGACTCAGTGATCGACTGCAATATGTCACCCAGAC
GGAAGCTTAATAGCGGGCTTTACCGGCGATTCGACTCAGTGATCGACTGCAATATGTCACCCAGAC
3690 3700 3710 3720 3730 3740 3750
4730 4740 4750 4760 4770 4780 4790
AGTCGACTTCAGCTGACCGGCTTTACCATTTGAGACCGACCGTGCACAAGACGGGTGTCAAGCTC
AGTCGACTTCAGCTGACCGGCTTTACCATTTGAGACCGACCGTGCACAAGACGGGTGTCAAGCTC
3760 3770 3780 3790 3800 3810 3820
4800 4810 4820 4830 4840 4850 4860
GCAAGCGGCGAGGAGTGGTGGGAGTGGGCAATTTACAGTTCGACTCCAGGAGACCGGCTCCTC
GCAAGCGGCGAGGAGTGGTGGGAGTGGGCAATTTACAGTTCGACTCCAGGAGACCGGCTCCTC
3830 3840 3850 3860 3870 3880 3890 3900
4870 4880 4890 4900 4910 4920 4930
GGGCAATTCGATTCCTCGGTCTGTCGAGTGTATGACCGGGGTGCTTGTGGTACAGCTCAGCCGCG
GGGCAATTCGATTCCTCGGTCTGTCGAGTGTATGACCGGGGTGCTTGTGGTACAGCTCAGCCGCG
3910 3920 3930 3940 3950 3960 3970
4940 4950 4960 4970 4980 4990 5000 5010
CGAGACTTCAGTTCGAGTTCGCGCTTACCTAAACACACAGGGTTCCTGTCGAGGACCATCTGGAGTT
CGAGACTTCAGTTCGAGTTCGCGCTTACCTAAACACACAGGGTTCCTGTCGAGGACCATCTGGAGTT
3980 3990 4000 4010 4020 4030 4040
5020 5030 5040 5050 5060 5070 5080
CTGGGAGAGCGTCTTTACAGGCTCACCACATAGAGCGCCATTTCTTGTCCAGACTAAGCAGGAGAGA
CTGGGAGAGCGTCTTTACAGGCTCACCACATAGAGCGCCATTTCTTGTCCAGACTAAGCAGGAGAGA
4050 4060 4070 4080 4090 4100 4110
5090 5100 5110 5120 5130 5140 5150
CAACTTCCCTACTCTGTAGTACACAGGCTAGCTGTGCGCAGGGCTCAGGCTCCACCTCCTGTTAGGCTGG
CAACTTCCCTACTCTGTAGTACACAGGCTAGCTGTGCGCAGGGCTCAGGCTCCACCTCCTGTTAGGCTGG
4120 4130 4140 4150 4160 4170 4180
5160 5170 5180 5190 5200 5210 5220
CCAAATGTGAAGTGTCTCATAGGCTTAAGCTTAGCTGCAAGGCGCAACGCCCTGCTGTATAGGCTGGG
CCAAATGTGAAGTGTCTCATAGGCTTAAGCTTAGCTGCAAGGCGCAACGCCCTGCTGTATAGGCTGGG
4190 4200 4210 4220 4230 4240 4250 4260
5230 5240 5250 5260 5270 5280 5290
AGCGGTCAAAAGAGGTATACACACACCCCAATACCAATATCATGTCATGTCATGTCGCTGACCT
AGCGGTCAAAAGAGGTATACACACACCCCAATACCAATATCATGTCATGTCATGTCGCTGACCT
4270 4280 4290 4300 4310 4320 4330
5300 5310 5320 5330 5340 5350 5360 5370
GGAAGTCTGTCACGAGCAGCTGGGTGCTGTGGTGGGAGTCTTAGAGCTCTGGCGGCTGCTGCAAC
GGAAGTCTGTCACGAGCAGCTGGGTGCTGTGGTGGGAGTCTTAGAGCTCTGGCGGCTGCTGCAAC
4340 4350 4360 4370 4380 4390 4400
5380 5390 5400 5410 5420 5430 5440
AGCAGCGTGGTCTTGTGGGAGGATCATTTGTCGGAAGCGCCCATCATTTCCGAGGAGTCTCT
AGCAGCGTGGTCTTGTGGGAGGATCATTTGTCGGAAGCGCCCATCATTTCCGAGGAGTCTCT
4410 4420 4430 4440 4450 4460 4470
5450 5460 5470 5480 5490 5500 5510

TTACCGGAGCTTCGATGAGATGGAAGTGGCCCTCACACCTCCTTACATCGAACAGGGAATGAGCTCGC
TTACCGGAGCTTCGATGAGATGGAAGTGGCCCTCACACCTCCTTACATCGAACAGGGAATGAGCTCGC
4480 4490 4500 4510 4520 4530 4540
5520 5530 5540 5550 5560 5570 5580
CGAAACATTCAAACAGAGGCAATCGGGTTGCTCGAAACAGCACCAGCAAGCGAGGCTGCTCTCCCGT
CGAAACATTCAAACAGAGGCAATCGGGTTGCTCGAAACAGCACCAGCAAGCGAGGCTGCTCTCCCGT
4550 4560 4570 4580 4590 4600 4610 4620
GGTGGAAATCCAAAGTGGCGGACCTTCGAAGCCCTTCGGCGAAGCATATGTGGAATTCATCAGCGGGATACA
4630 4640 4650 4660 4670 4680 4690
5590 5600 5610 5620 5630 5640 5650
GGTGGAAATCCAAAGTGGCGGACCTTCGAAGCCCTTCGGCGAAGCATATGTGGAATTCATCAGCGGGATACA
4630 4640 4650 4660 4670 4680 4690
5660 5670 5680 5690 5700 5710 5720 5730
ATATTTAGCAGGCTTGCCACTCTGCTGCGCAACCCCGCATAGCATCACTGATGGCATTCACAGCCCTTAT
ATATTTAGCAGGCTTGCCACTCTGCTGCGCAACCCCGCATAGCATCACTGATGGCATTCACAGCCCTTAT
4700 4710 4720 4730 4740 4750 4760
5740 5750 5760 5770 5780 5790 5800
CACCAGCCGCTCACCAACCAACATACCTCTGTTTAAACATCTCGGGGGATGGTGCGGCCCAACTTGC
CACCAGCCGCTCACCAACCAACATACCTCTGTTTAAACATCTCGGGGGATGGTGCGGCCCAACTTGC
4770 4780 4790 4800 4810 4820 4830
TCTCCAGCGCTGCTTCGCTTCTGAGGCGCGGCATCGCTGAGCGGCTGTGGCAGCATAGGCGCTTGG
4840 4850 4860 4870 4880 4890 4900
5880 5890 5900 5910 5920 5930 5940
GAGGTGCTTGTGATATTTGGAGGTTATGGAGCAGGGGTGGCAGCGGCTGTGGCCTTTAAGGTAT
GAGGTGCTTGTGATATTTGGAGGTTATGGAGCAGGGGTGGCAGCGGCTGTGGCCTTTAAGGTAT
4910 4920 4930 4940 4950 4960 4970 4980 4990
5950 5960 5970 5980 5990 6000 6010
GAGGGCGAGTGCCTCCACCGAGGACCTGGTAAACCTACTCCCTGCTATCTCTCCCTGGCGCCCTAGT
GAGGGCGAGTGCCTCCACCGAGGACCTGGTAAACCTACTCCCTGCTATCTCTCCCTGGCGCCCTAGT
4990 5000 5010 5020 5030 5040 5050
6020 6030 6040 6050 6060 6070 6080 6090
CGTGGGTCGTGTCGCGAGCATACTCGCTCGGCACCTGGCCACAGGGGGGGGCTGTGAGTGGATGA
CGTGGGTCGTGTCGCGAGCATACTCGCTCGGCACCTGGCCACAGGGGGGGGCTGTGAGTGGATGA
5060 5070 5080 5090 5100 5110 5120
6100 6110 6120 6130 6140 6150 6160
CCGCTGATAGCTTCGCTTCGGGGTAAACAGCTCTCCCGCAGCACTATGCTGCTGAGAGCGAGCTGC
CCGCTGATAGCTTCGCTTCGGGGTAAACAGCTCTCCCGCAGCACTATGCTGCTGAGAGCGAGCTGC
5130 5140 5150 5160 5170 5180 5190
6170 6180 6190 6200 6210 6220 6230
AGACGTCCTACTGATCTCTTACCTTACCTACTAGCTGCTGAAAGAGCTTACCAAGTGGATCAA
AGACGTCCTACTGATCTCTTACCTTACCTACTAGCTGCTGAAAGAGCTTACCAAGTGGATCAA
5200 5210 5220 5230 5240 5250 5260
6240 6250 6260 6270 6280 6290 6300
CGAGGACTGCTCCAGCCCATCTCCGGCTCGTGGCTAAGAGATGTTGGATGATGACAGCTGTTGAC
CGAGGACTGCTCCAGCCCATCTCCGGCTCGTGGCTAAGAGATGTTGGATGATGACAGCTGTTGAC
5270 5280 5290 5300 5310 5320 5330 5340
6310 6320 6330 6340 6350 6360 6370
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TGATTTCAAGGCTCGCTCCAGTCCAGCTCTCGCGGAGTTCCGGGGAGTCCCTTCTTCTCATGTCAACG
5350 5360 5370 5380 5390 5400 5410
6380 6390 6400 6410 6420 6430 6440 6450
TGGGTACAAGGAGTCTGCGGGGCGACGGCATATGCAAAACCACTCCCATGTGGAGCACAGATCACCGG
TGGGTACAAGGAGTCTGCGGGGCGACGGCATATGCAAAACCACTCCCATGTGGAGCACAGATCACCGG
5420 5430 5440 5450 5460 5470 5480
6460 6470 6480 6490 6500 6510 6520
ACATGTGAAAAACGGTTCATGAGATCTGGGGCTTAGACCTTAGTAAACAGCTGGCATGGAATTTCCC
ACATGTGAAAAACGGTTCATGAGATCTGGGGCTTAGGACCTTAGTAAACAGCTGGCATGGAATTTCCC
5490 5500 5510 5520 5530 5540 5550
6530 6540 6550 6560 6570 6580 6590
CATTAACGGTACACACCGGCTTCGACCGCTCCCGCGGCGCAAAATTTCTAGGGCGTGTGGCGGT
CATTAACGGTACACACCGGCTTCGACCGCTCCCGCGGCGCAAAATTTCTAGGGCGTGTGGCGGT
5560 5570 5580 5590 5600 5610 5620
6600 6610 6620 6630 6640 6650 6660
GGCTGCTGAGGAGTACGTGGAGGTTACCGGGTGGGGATTTCCACTAGTACCGGCAATGACCTGACAA
GGCTGCTGAGGAGTACGTGGAGGTTACCGGGTGGGGATTTCCACTAGTACCGGCAATGACCTGACAA
5630 5640 5650 5660 5670 5680 5690 5700 5710
CGTAAAGTCCCGTGTGAGTTCGGGCTCCCGCCCGAAATTTCTTCAAGAAAGTGGATGGGGTGGTGCACAGTA
5710 5720 5730 5740 5750 5760 5770
6740 6750 6760 6770 6780 6790 6800 6810
CGCTCAGGTCGAAACCCCTCTACGGGAGGAGTCAATTCCTGGTGGGCTCAATCAATCTGTGTGG
CGCTCAGGTCGAAACCCCTCTACGGGAGGAGTCAATTCCTGGTGGGCTCAATCAATCTGTGTGG
5780 5790 5800 5810 5820 5830 5840
6820 6830 6840 6850 6860 6870 6880
GTCAAGCTTCCTTCCAGCCCGCAACCGGACGTAGCAGTGTCACTTCCATGCTCAACCCCTCCACAT
GTCAAGCTTCCTTCCAGCCCGCAACCGGACGTAGCAGTGTCACTTCCATGCTCAACCCCTCCACAT
5850 5860 5870 5880 5890 5900 5910
6890 6900 6910 6920 6930 6940 6950
TACGGCGGAGAGCGCTTAAGCTAGGTCGCGGAGGATCTCCCTCTTGGCCAGCTCATCAGTAGCCA
TACGGCGGAGAGCGCTTAAGCTAGGTCGCGGAGGATCTCCCTCTTGGCCAGCTCATCAGTAGCCA
5920 5930 5940 5950 5960 5970 5980
6960 6970 6980 6990 7000 7010 7020
GCTGTCTGCGCTTCTTGAAGCAACATGCACTACCGCTCATGACTCCCGGAGCTGACCTCATCGAGGC
GCTGTCTGCGCTTCTTGAAGCAACATGCACTACCGCTCATGACTCCCGGAGCTGACCTCATCGAGGC
5990 6000 6010 6020 6030 6040 6050 6060
7030 7040 7050 7060 7070 7080 7090
CAACCTCTGTGGCGGAGAGTGGCGGGAACATCACCGGCTGGAGTCAGAGTAAGTAGTAATTTT
CAACCTCTGTGGCGGAGAGTGGCGGGAACATCACCGGCTGGAGTCAGAGTAAGTAGTAATTTT
6070 6080 6090 6100 6110 6120 6130
7100 7110 7120 7130 7140 7150 7160 7170
GGACTCTTTCGAGCGCTTCCAGCGGAGGATGAGAGGAGTATCCGTTCCGGGAGATCTTCGCGGAG
GGACTCTTTCGAGCGCTTCCAGCGGAGGATGAGAGGAGTATCCGTTCCGGGAGATCTTCGCGGAG
6140 6150 6160 6170 6180 6190 6200
7180 7190 7200 7210 7220 7230 7240
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GTGTTGACCTGTCTATCATGTGCGGCTCAAAGACCTTGC CGGCCCAAGGGGCCCAATCACCCAAATGTA
 GTGTTGACCTGTCTATCATGTGCGGCTCAAAGACCTTGC CGGCCCAAGGGGCCCAATCACCCAAATGTA
 2610 2620 2630 2640 2650 2660 2670
 3650 3660 3670 3680 3690 3700 3710
 CAGCAATGTGGACGAGACCTCTGTGCGGTGCAAGCGCCCGCGGGCGGTTCCTTGACACCATGCGACCTG
 CACCAATGTGGACGAGACCTCTGTGCGGTGCAAGCGCCCGCGGGCGGTTCCTTGACACCATGCGACCTG
 2680 2690 2700 2710 2720 2730 2740
 3720 3730 3740 3750 3760 3770 3780
 CGGACGCTCGGACCTTTACTTGTGTCAGGAGCAGCCGATGTCAATTCGCGGTGCGCGGGCGGCGACGACG
 CGGACGCTCGGACCTTTACTTGTGTCAGGAGCAGCCGATGTCAATTCGCGGTGCGCGGGCGGCGACGACG
 2750 2760 2770 2780 2790 2800 2810 2820
 3790 3800 3810 3820 3830 3840 3850
 GGGAGGCTACTCTCTCCCGGCGGCTCTCTCTACTTGAAGGCTCTTGGGGCGGTCCACTGTCTGCGCCCTC
 GGGAGGCTACTCTCTCCCGGCGGCTCTCTCTACTTGAAGGCTCTTGGGGCGGTCCACTGTCTGCGCCCTC
 2830 2840 2850 2860 2870 2880 2890
 3860 3870 3880 3890 3900 3910 3920 3930
 GGGAGGCTACTCTCTCCCGGCGGCTCTCTCTACTTGAAGGCTCTTGGGGCGGTCCACTGTCTGCGCCCTC
 GGGAGGCTACTCTCTCCCGGCGGCTCTCTCTACTTGAAGGCTCTTGGGGCGGTCCACTGTCTGCGCCCTC
 2900 2910 2920 2930 2940 2950 2960
 3940 3950 3960 3970 3980 3990 4000
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3580	3590	3600	3610	3620	3630	3640	3650
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3680	3690	3700	3710	3720	3730	3740	3750
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3680	3690	3700	3710	3720	3730	3740	3750
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3680	3690	3700	3710	3720	3730	3740	3750
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3680	3690	3700	3710	3720	3730	3740	3750
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3680	3690	3700	3710	3720	3730	3740	3750
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3680	3690	3700	3710	3720	3730	3740	3750
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3680	3690	3700	3710	3720	3730	3740	3750
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4220 4230 4240 4250 4260 4270 4280 4290
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